



## SEQUENCE LISTING

<110> Waldman, Scott A.  
Pearlman, Joshua M.  
Barber, Michael T.  
Schulz, Stephanie  
Parkinson, Scott J.

<120> Compositions that Specifically Bind to Colorectal Cancer Cells  
and Methods of Using the Same

<130> 08321-0152 CT1 (TJU0007-103)

<140> 10/656,895  
<141> 2003-09-05

<150> US 09/649,697  
<151> 2000-08-28

<150> US 08/908,643  
<151> 1997-08-07

<160> 82

<170> PatentIn version 3.3

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240

gctgtgtcct catagggccc tcatgtacat actccacctt ccagatgtac cttgacacag  
300

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aaaccaacga tctgcccttc aaaacttatt cctggagcac ttcgtatggt tacaagaatg  
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840

accaacaaaa cgagactttg ctcttgccata tttgaatgga atcctgctct ttggacatat  
900

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960

caggaatctc acttttgaag ggtatgacgg tccagtgacc ttgggatgac tggggggatg  
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cagaaaatat agaaaagatt atgaacttcg tcagaaaaaa tgggtcccaca ttctctctga  
1320

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tccttttagtt cccaggcc  
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Met Lys Thr Leu Leu Leu Asp Leu Ala Leu Trp Ser Leu Leu Phe His  
1 5 10 15

Pro Gly Trp Leu Ser Phe Ser Ser Gln Ala  
20 25

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<211> 372  
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120

tcattgtacat actccacctt ccagatgtac cttgacacag aattgagcta ccccatgatc  
180

tcagctggaa gttttggatt gtcattgtgac tataaagaaa ccttaaccag gctgatgtct  
240

ccagctgaga agttgatata cttcttggtt aacttttgga aaaccaacga tctgcccttc  
300

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Met Tyr Ser Asp Gly Leu Ile His Asn Ser Gly Asp Cys Arg Ser Ser  
1 5 10 15

Thr Cys Glu Gly Leu Asp Leu Leu Arg Lys Ile Ser Asn Ala Gln Arg  
20 25 30

Met Gly Cys Val Leu Ile Gly Pro Ser Cys Thr Tyr Ser Thr Phe Gln  
35 40 45

Met Tyr Leu Asp Thr Glu Leu Ser Tyr Pro Met Ile Ser Ala Gly Ser  
50 55 60

Phe Gly Leu Ser Cys Asp Tyr Lys Glu Thr Leu Thr Arg Leu Met Ser  
65 70 75 80

Pro Ala Arg Lys Leu Ile Tyr Phe Leu Val Asn Phe Trp Lys Thr Asn  
85 90 95

Asp Leu Pro Phe Lys Thr Tyr Ser Trp Ser Thr Ser Tyr Val Tyr Lys  
100 105 110

Asn Gly Thr Glu Thr Glu Gly Leu Phe Leu Val Pro  
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120

gaaaccttaa ccaggctgat gtctccagct agaaagttga tatacttctt ggtaacttt  
180

tggaaaacca acgatctgcc cttcaaaact tattcctgga gcacttcgta tgtttacaag  
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aatggtacag aaactgaggg actgtttctg gtacct  
276

<210> 7

<211> 92

<212> PRT

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<220>

<223> Synthetic Construct

<400> 7

Met	Gly	Cys	Val	Leu	Ile	Gly	Pro	Ser	Cys	Thr	Tyr	Ser	Thr	Phe	Gln
1				5					10					15	

Met	Tyr	Leu	Asp	Thr	Glu	Leu	Ser	Tyr	Pro	Met	Ile	Ser	Ala	Gly	Ser
			20					25					30		

Phe	Gly	Leu	Ser	Cys	Asp	Tyr	Lys	Glu	Thr	Leu	Thr	Arg	Leu	Met	Ser
		35					40					45			

Pro	Ala	Arg	Lys	Leu	Ile	Tyr	Phe	Leu	Val	Asn	Phe	Trp	Lys	Thr	Asn
	50					55					60				

Asp Leu Pro Phe Lys Thr Tyr Ser Trp Ser Thr Ser Tyr Val Tyr Lys  
65 70 75 80

Asn Gly Thr Glu Thr Glu Gly Leu Phe Leu Val Pro  
85 90

<210> 8  
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tgtgactata aagaaacctt aaccaggctg atgtctccag ctagaaagtt gatatacttc  
120

ttggttaact tttggaaaac caacgatctg cccttcaaaa cttattcctg gagcacttcg  
180

tatgtttaca agaatgggtac agaaactgag ggactgtttc tgggtacct  
228

<210> 9  
<211> 76  
<212> PRT  
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<220>  
<223> Synthetic Construct

<400> 9

Met Tyr Leu Asp Thr Glu Leu Ser Tyr Pro Met Ile Ser Ala Gly Ser  
1 5 10 15

Phe Gly Leu Ser Cys Asp Tyr Lys Glu Thr Leu Thr Arg Leu Met Ser  
20 25 30

Pro Ala Arg Lys Leu Ile Tyr Phe Leu Val Asn Phe Trp Lys Thr Asn  
35 40 45

Asp Leu Pro Phe Lys Thr Tyr Ser Trp Ser Thr Ser Tyr Val Tyr Lys  
50 55 60

Asn Gly Thr Glu Thr Glu Gly Leu Phe Leu Val Pro  
65 70 75

<210> 10  
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<220>  
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atgtctccag ctagaaagtt gatatacttc ttggttaact tttggaaaac caacgatctg  
120

cccttcaaaa cttattcctg gagcacttcg tatgtttaca agaatgggtac agaaactgag  
180

ggactgtttc tggtagct  
198

<210> 11  
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<220>  
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<400> 11

Met Ile Ser Ala Gly Ser Phe Gly Leu Ser Cys Asp Tyr Lys Glu Thr  
1 5 10 15

Leu Thr Arg Leu Met Ser Pro Ala Arg Lys Leu Ile Tyr Phe Leu Val  
20 25 30

Asn Phe Trp Lys Thr Asn Asp Leu Pro Phe Lys Thr Tyr Ser Trp Ser  
35 40 45

Thr Ser Tyr Val Tyr Lys Asn Gly Thr Glu Thr Glu Gly Leu Phe Leu  
50 55 60

Val Pro  
65

<210> 12

<211> 138

<212> DNA

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<220>

<223> Synthetic Construct

<400> 12

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120

ggactgtttc tggtagct  
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<210> 13

<211> 46

<212> PRT

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<220>

<223> Synthetic Construct

<400> 13

Met	Ser	Pro	Ala	Arg	Lys	Leu	Ile	Tyr	Phe	Leu	Val	Asn	Phe	Trp	Lys
1				5					10					15	

Thr	Asn	Asp	Leu	Pro	Phe	Lys	Thr	Tyr	Ser	Trp	Ser	Thr	Ser	Tyr	Val
			20					25					30		

Tyr	Lys	Asn	Gly	Thr	Glu	Thr	Glu	Gly	Leu	Phe	Leu	Val	Pro
		35					40					45	

<210> 14

<211> 27

<212> DNA

<213> Artificial Sequence

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27

<210> 15

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 15

Met	His	Asn	Gly	Trp	Ala	Val	Ser	Ser
1				5				

<210> 16

<211> 30

<212> DNA  
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<210> 17  
 <211> 10  
 <212> PRT  
 <213> Artificial Sequence  
 <220>  
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 <400> 17

Met	Tyr	Ile	Leu	His	Leu	Pro	Asp	Val	Pro
1				5					10

<210> 18  
 <211> 351  
 <212> DNA  
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 <220>  
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 120

gagtttcagg atatcttaat ggaccacaac aggaaaagca atgtgattat tatgtgtggt  
 180

ggtccagagt tcctctacaa gctgaagggt gaccgagcag tggctgaaga cattgtcatt  
 240

attctagtgg atcttttcaa tgaccagtac ttggaggaca atgtcacagc ccctgactat  
300

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351

<210> 19

<211> 117

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<400> 19

Met Phe Thr Arg Met Val Gln Lys Leu Arg Asp Cys Phe Trp Tyr Leu  
1 5 10 15

Asn Ala Leu Glu Ala Ser Val Ser Tyr Phe Ser His Glu Leu Gly Phe  
20 25 30

Lys Val Val Leu Arg Gln Asp Lys Glu Phe Gln Asp Ile Leu Met Asp  
35 40 45

His Asn Arg Lys Ser Asn Val Ile Ile Met Cys Gly Gly Pro Glu Phe  
50 55 60

Leu Tyr Lys Leu Lys Gly Asp Arg Ala Val Ala Glu Asp Ile Val Ile  
65 70 75 80

Ile Leu Val Asp Leu Phe Asn Asp Gln Tyr Leu Glu Asp Asn Val Thr  
85 90 95

Ala Pro Asp Tyr Met Lys Asn Val Leu Val Leu Thr Leu Ser Pro Gly  
100 105 110

Glu Phe Pro Ser Lys

<210> 20  
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 120

atcttaatgg accacaacag gaaaagcaat gtgattatta tgtgtggtgg tccagagttc  
 180

ctctacaagc tgaaggggtga ccgagcagtg gctgaagaca ttgtcattat tctagtggat  
 240

cttttcaatg accagtactt ggaggacaat gtcacagccc ctgactatat gaaaaatgtc  
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cttgttctga cgctgtctcc tggggaattc ccttctaaa  
 339

<210> 21  
 <211> 113  
 <212> PRT  
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<220>  
 <223> Synthetic Construct

<400> 21

Met	Val	Gln	Lys	Leu	Arg	Asp	Cys	Phe	Trp	Tyr	Leu	Asn	Ala	Leu	Glu
1				5					10					15	

Ala	Ser	Val	Ser	Tyr	Phe	Ser	His	Glu	Leu	Gly	Phe	Lys	Val	Val	Leu
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

20

25

30

Arg Gln Asp Lys Glu Phe Gln Asp Ile Leu Met Asp His Asn Arg Lys  
           35                          40                          45

Ser Asn Val Ile Ile Met Cys Gly Gly Pro Glu Phe Leu Tyr Lys Leu  
       50                          55                          60

Lys Gly Asp Arg Ala Val Ala Glu Asp Ile Val Ile Ile Leu Val Asp  
   65                          70                          75                          80

Leu Phe Asn Asp Gln Tyr Leu Glu Asp Asn Val Thr Ala Pro Asp Tyr  
                           85                          90                          95

Met Lys Asn Val Leu Val Leu Thr Leu Ser Pro Gly Glu Phe Pro Ser  
                           100                          105                          110

Lys

<210> 22  
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<400> 22  
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aatgaccagt acttgaggga caatgtcaca gccctgact atatgaaaaa tgtccttggt  
 180

ctgacgctgt ctcctgggga attcccttct aaa

213

<210> 23  
<211> 71  
<212> PRT  
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<400> 23

Met Asp His Asn Arg Lys Ser Asn Val Ile Ile Met Cys Gly Gly Pro  
1 5 10 15

Glu Phe Leu Tyr Lys Leu Lys Gly Asp Arg Ala Val Ala Glu Asp Ile  
20 25 30

Val Ile Ile Leu Val Asp Leu Phe Asn Asp Gln Tyr Leu Glu Asp Asn  
35 40 45

Val Thr Ala Pro Asp Tyr Met Lys Asn Val Leu Val Leu Thr Leu Ser  
50 55 60

Pro Gly Glu Phe Pro Ser Lys  
65 70

<210> 24  
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<212> DNA  
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<400> 24

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attgtcatta ttctagtgga tcttttcaat gaccagtact tggaggacaa tgtcacagcc

120

cctgactata tgaaaaatgt ccttggttctg acgctgtctc ctggggaatt cccttctaaa  
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<210> 25

<211> 60

<212> PRT

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<223> Synthetic Construct

<400> 25

Met	Cys	Gly	Gly	Pro	Glu	Phe	Leu	Tyr	Lys	Leu	Lys	Gly	Asp	Arg	Ala
1				5					10					15	

Val	Ala	Glu	Asp	Ile	Val	Ile	Ile	Leu	Val	Asp	Leu	Phe	Asn	Asp	Gln
			20					25						30	

Tyr	Leu	Glu	Asp	Asn	Val	Thr	Ala	Pro	Asp	Tyr	Met	Lys	Asn	Val	Leu
		35					40					45			

Val	Leu	Thr	Leu	Ser	Pro	Gly	Glu	Phe	Pro	Ser	Lys
	50					55					60

<210> 26

<211> 51

<212> DNA

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<400> 26

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51

<210> 27



<211> 17  
<212> PRT  
<213> Artificial Sequence

<220>  
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<400> 27

Met	Lys	Asn	Val	Leu	Val	Leu	Thr	Leu	Ser	Pro	Gly	Glu	Phe	Pro	Ser
1			5					10						15	

Lys

<210> 28  
<211> 57  
<212> DNA  
<213> Artificial Sequence

<220>  
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<400> 28  
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57

<210> 29  
<211> 19  
<212> PRT  
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<400> 29

Met	Leu	Trp	Arg	Leu	Ala	Phe	Pro	Ile	Ser	Pro	Thr	Asn	Ser	Ala	Leu
1				5					10					15	

Arg Trp Cys

<210> 30  
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<212> DNA  
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<400> 30  
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42

<210> 31  
<211> 14  
<212> PRT  
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<220>  
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<400> 31

Met	Thr	Ser	Thr	Trp	Arg	Thr	Met	Ser	Gln	Pro	Leu	Thr	Ile
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<210> 32  
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<212> DNA  
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<400> 32  
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<210> 33  
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<223> Synthetic Construct

<400> 33

Met Ser Gln Pro Leu Thr Ile  
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<210> 34

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 34

atggaatcct gctcttttgga catatgc  
27

<210> 35

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 35

Met Glu Ser Cys Ser Leu Asp Ile Cys  
1 5

<210> 36

<211> 108

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 36

atgctgaaga tatttcttga aaatggagaa aatattacca cccccaaatt tgctcatgct  
60

ttcaggaatc tcacttttga agggatatgac ggtccagtga ccttgggga  
108

<210> 37  
<211> 36  
<212> PRT  
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<220>  
<223> Synthetic Construct

<400> 37

Met	Leu	Lys	Ile	Phe	Leu	Glu	Asn	Gly	Glu	Asn	Ile	Thr	Thr	Pro	Lys
1				5					10					15	

Phe	Ala	His	Ala	Phe	Arg	Asn	Leu	Thr	Phe	Glu	Gly	Tyr	Asp	Gly	Pro
			20					25						30	

Val	Thr	Leu	Gly
			35

<210> 38  
<211> 75  
<212> DNA  
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<223> Synthetic Construct

<400> 38

atggagaaaa tattaccacc cccaaatttg ctcatgcttt caggaatctc acttttgaag  
60

ggtatgacgg tccag  
75

<210> 39

<211> 25  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic Construct

<400> 39

Met Glu Lys Ile Leu Pro Pro Pro Asn Leu Leu Met Leu Ser Gly Ile  
1 5 10 15

Ser Leu Leu Lys Gly Met Thr Val Gln  
20 25

<210> 40  
<211> 42  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Construct

<400> 40  
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42

<210> 41  
<211> 14  
<212> PRT  
<213> Artificial Sequence

<220>  
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<400> 41

Met Leu Ser Gly Ile Ser Leu Leu Lys Gly Met Thr Val Gln  
1 5 10

<210> 42  
<211> 84

<212> DNA  
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 <220>  
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 60

gaaatacaag gttcttttggga ccta  
 84

<210> 43  
 <211> 28  
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<220>  
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<400> 43

Met	Thr	Gly	Gly	Met	Leu	Thr	Val	Pro	Trp	Cys	Phe	Arg	Tyr	Thr	Leu
1				5					10					15	

Cys	Gly	His	Gln	Glu	Ile	Gln	Gly	Ser	Leu	Asp	Leu
			20					25			

<210> 44  
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 <212> DNA  
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<220>  
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<400> 44  
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 60

tcttttgacc ta  
 72

<210> 45  
<211> 24  
<212> PRT  
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<223> Synthetic Construct

<400> 45

Met	Leu	Thr	Val	Pro	Trp	Cys	Phe	Arg	Tyr	Thr	Leu	Cys	Gly	His	Gln
1				5					10					15	

Glu	Ile	Gln	Gly	Ser	Leu	Asp	Leu
			20				

<210> 46  
<211> 93  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Construct

<400> 46  
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60

ataccacgt taataagaac ttcctgtgg ata  
93

<210> 47  
<211> 31  
<212> PRT  
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<220>  
<223> Synthetic Construct

<400> 47

Met Val Leu Pro Leu Tyr Pro Leu Trp Thr Pro Arg Asn Thr Arg Phe  
1 5 10 15

Phe Gly Pro Met Ile Pro Thr Leu Ile Arg Thr Ile Leu Trp Ile  
20 25 30

<210> 48  
<211> 36  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Construct

<400> 48  
atgataccca cgtaataag aactatcctg tggata  
36

<210> 49  
<211> 12  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic Construct

<400> 49

Met Ile Pro Thr Leu Ile Arg Thr Ile Leu Trp Ile  
1 5 10

<210> 50  
<211> 498  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Construct

<400> 50  
atgagcccca cattcacttg gaagaactct aaacttccta atgatattac aggccggggc  
60



cctcagatcc tgatgattgc agtcttcacc ctccactggag ctgtgggtgct gctcctgctc  
120

gtcgctctcc tgatgctcag aaaatataga aaagattatg aacttcgtca gaaaaaatgg  
180

tcccacattc ctccctgaaaa tatctttcct ctggagacca atgagaccaa tcatgttagc  
240

ctcaagatcg atgatgacaa aagacgagat acaatccaga gactacgaca gtgcaaatac  
300

gacaaaaagc gagtgattct caaagatctc aagcacaatg atggtaattt cactgaaaaa  
360

cagaagatag aattgaacaa gttgcttcag aaagactatt acaacctgac caagttctac  
420

ggcacagtga aacttgatac catgatcttc ggggtgatag aatactgtga gagaggatcc  
480

cctccgggaa gttttaaa  
498

<210> 51  
<211> 166  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic Construct

<400> 51

Met	Ser	Pro	Thr	Phe	Thr	Trp	Lys	Asn	Ser	Lys	Leu	Pro	Asn	Asp	Ile
1				5					10					15	

Thr	Gly	Arg	Gly	Pro	Gln	Ile	Leu	Met	Ile	Ala	Val	Phe	Thr	Leu	Thr
			20					25						30	

Gly	Ala	Val	Val	Leu	Leu	Leu	Leu	Val	Ala	Leu	Leu	Met	Leu	Arg	Lys
		35					40					45			

Tyr Arg Lys Asp Tyr Glu Leu Arg Gln Lys Lys Trp Ser His Ile Pro  
50 55 60

Pro Glu Asn Ile Phe Pro Leu Glu Thr Asn Glu Thr Asn His Val Ser  
65 70 75 80

Leu Lys Ile Asp Asp Asp Lys Arg Arg Asp Thr Ile Gln Arg Leu Arg  
85 90 95

Gln Cys Lys Tyr Asp Lys Lys Arg Val Ile Leu Lys Asp Leu Lys His  
100 105 110

Asn Asp Gly Asn Phe Thr Glu Lys Gln Lys Ile Glu Leu Asn Lys Leu  
115 120 125

Leu Gln Lys Asp Tyr Tyr Asn Leu Thr Lys Phe Tyr Gly Thr Val Lys  
130 135 140

Leu Asp Thr Met Ile Phe Gly Val Ile Glu Tyr Cys Glu Arg Gly Ser  
145 150 155 160

Pro Pro Gly Ser Phe Lys  
165

<210> 52  
<211> 426  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Construct

<400> 52  
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60

atgctcagaa aatatagaaa agattatgaa cttcgtcaga aaaaatggtc ccacattcct  
120

cctgaaaata tctttcctct ggagaccaat gagaccaatc atgttagcct caagatcgat  
180

gatgacaaaa gacgagatac aatccagaga ctacgacagt gcaaatacga caaaaagcga  
240

gtgattctca aagatctcaa gcacaatgat ggtaatttca ctgaaaaaca gaagatagaa  
300

ttgaacaagt tgcttcagaa agactattac aacctgacca agttctacgg cacagtgaaa  
360

cttgatacca tgatcttcgg ggtgatagaa tactgtgaga gaggatcccc tccgggaagt  
420

tttaaa  
426

<210> 53  
<211> 142  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic Construct

<400> 53

Met Ile Ala Val Phe Thr Leu Thr Gly Ala Val Val Leu Leu Leu Leu  
1 5 10 15

Val Ala Leu Leu Met Leu Arg Lys Tyr Arg Lys Asp Tyr Glu Leu Arg  
20 25 30

Gln Lys Lys Trp Ser His Ile Pro Pro Glu Asn Ile Phe Pro Leu Glu  
35 40 45

Thr Asn Glu Thr Asn His Val Ser Leu Lys Ile Asp Asp Asp Lys Arg  
50 55 60

Arg Asp Thr Ile Gln Arg Leu Arg Gln Cys Lys Tyr Asp Lys Lys Arg  
65 70 75 80

Val Ile Leu Lys Asp Leu Lys His Asn Asp Gly Asn Phe Thr Glu Lys  
85 90 95

Gln Lys Ile Glu Leu Asn Lys Leu Leu Gln Lys Asp Tyr Tyr Asn Leu  
100 105 110

Thr Lys Phe Tyr Gly Thr Val Lys Leu Asp Thr Met Ile Phe Gly Val  
115 120 125

Ile Glu Tyr Cys Glu Arg Gly Ser Pro Pro Gly Ser Phe Lys  
130 135 140

<210> 54  
<211> 366  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Construct

<400> 54  
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60

cctgaaaata tctttcctct ggagaccaat gagaccaatc atgttagcct caagatcgat  
120

gatgacaaaa gacgagatac aatccagaga ctacgacagt gcaaatacga caaaaagcga  
180

gtgattctca aagatctcaa gcacaatgat ggtaatttca ctgaaaaaca gaagatagaa  
240

ttgaacaagt tgcttcagaa agactattac aacctgacca agttctacgg cacagtgaaa  
300

cttgatacca tgatcttcgg ggtgatagaa tactgtgaga gaggatcccc tccgggaagt  
360

tttaaa  
366

<210> 55  
<211> 122  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic Construct

<400> 55

Met Leu Arg Lys Tyr Arg Lys Asp Tyr Glu Leu Arg Gln Lys Lys Trp  
1 5 10 15

Ser His Ile Pro Pro Glu Asn Ile Phe Pro Leu Glu Thr Asn Glu Thr  
20 25 30

Asn His Val Ser Leu Lys Ile Asp Asp Asp Lys Arg Arg Asp Thr Ile  
35 40 45

Gln Arg Leu Arg Gln Cys Lys Tyr Asp Lys Lys Arg Val Ile Leu Lys  
50 55 60

Asp Leu Lys His Asn Asp Gly Asn Phe Thr Glu Lys Gln Lys Ile Glu  
65 70 75 80

Leu Asn Lys Leu Leu Gln Lys Asp Tyr Tyr Asn Leu Thr Lys Phe Tyr  
85 90 95

Gly Thr Val Lys Leu Asp Thr Met Ile Phe Gly Val Ile Glu Tyr Cys  
100 105 110

Glu Arg Gly Ser Pro Pro Gly Ser Phe Lys

115

120

<210> 56  
<211> 57  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Construct

<400> 56  
atgatcttcg gggatgata atactgtgag agaggatccc ctccgggaag ttttaaa  
57

<210> 57  
<211> 19  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic Construct

<400> 57

Met	Ile	Phe	Gly	Val	Ile	Glu	Tyr	Cys	Glu	Arg	Gly	Ser	Pro	Pro	Gly
1				5					10					15	

Ser Phe Lys

<210> 58  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Construct

<400> 58  
atgatattac aggcgggggc cctcagatcc  
30

<210> 59  
<211> 10  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic Construct

<400> 59

Met Ile Leu Gln Ala Gly Ala Leu Arg Ser  
1 5 10

<210> 60  
<211> 156  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Construct

<400> 60

atgaacttcg tcagaaaaaa tgggtcccaca ttctctctga aaatatcttt cctctggaga  
60

ccaatgagac caatcatgtt agcctcaaga tcgatgatga caaaagacga gatacaatcc  
120

agagactacg acagtgcaaa tacgacaaaa agcgag  
156

<210> 61  
<211> 52  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic Construct

<400> 61

Met Asn Phe Val Arg Lys Asn Gly Pro Thr Phe Leu Leu Lys Ile Ser  
1 5 10 15

Phe Leu Trp Arg Pro Met Arg Pro Ile Met Leu Ala Ser Arg Ser Met  
20 25 30

Met Thr Lys Asp Glu Ile Gln Ser Arg Asp Tyr Asp Ser Ala Asn Thr  
35 40 45

Thr Lys Ser Glu  
50

<210> 62  
<211> 93  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Construct

<400> 62  
atgagaccaa tcattgttagc ctcaagatcg atgatgacaa aagacgagat acaatccaga  
60

gactacgaca gtgcaaatac gacaaaaagc gag  
93

<210> 63  
<211> 31  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic Construct

<400> 63

Met Arg Pro Ile Met Leu Ala Ser Arg Ser Met Met Thr Lys Asp Glu  
1 5 10 15

Ile Gln Ser Arg Asp Tyr Asp Ser Ala Asn Thr Thr Lys Ser Glu  
20 25 30



<210> 64  
<211> 81  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Construct

<400> 64  
atgttagcct caagatcgat gatgacaaaa gacgagatac aatccagaga ctacgacagt  
60

gcaaatacga caaaaagcga g  
81

<210> 65  
<211> 27  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic Construct

<400> 65

Met	Leu	Ala	Ser	Arg	Ser	Met	Met	Thr	Lys	Asp	Glu	Ile	Gln	Ser	Arg
1				5					10					15	

Asp	Tyr	Asp	Ser	Ala	Asn	Thr	Thr	Lys	Ser	Glu
			20					25		

<210> 66  
<211> 63  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Construct

<400> 66  
atgatgacaa aagacgagat acaatccaga gactacgaca gtgcaaatac gacaaaaagc

60

gag  
63

<210> 67  
<211> 21  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic Construct

<400> 67

Met	Met	Thr	Lys	Asp	Glu	Ile	Gln	Ser	Arg	Asp	Tyr	Asp	Ser	Ala	Asn
1				5					10					15	

Thr	Thr	Lys	Ser	Glu
				20

<210> 68  
<211> 60  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Construct

<400> 68

atgacaaaag acgagataca atccagagac tacgacagtg caaatacgac aaaaagcgag  
60

<210> 69  
<211> 20  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic Construct

<400> 69

Met Thr Lys Asp Glu Ile Gln Ser Arg Asp Tyr Asp Ser Ala Asn Thr  
1 5 10 15

Thr Lys Ser Glu  
20

<210> 70  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Construct

<400> 70  
atggtccac attcctcc  
18

<210> 71  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic Construct

<400> 71

Met Val Pro His Ser Ser  
1 5

<210> 72  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Construct

<400> 72  
atgatggttaa tttcactgaa aaacagaaga

30

<210> 73  
<211> 10  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic Construct

<400> 73

Met	Met	Val	Ile	Ser	Leu	Lys	Asn	Arg	Arg
1				5					10

<210> 74  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Construct

<400> 74  
atggtaattt cactgaaaaa cagaaga  
27

<210> 75  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic Construct

<400> 75

Met	Val	Ile	Ser	Leu	Lys	Asn	Arg	Arg
1				5				

<210> 76  
<211> 42

<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic Construct  
  
<400> 76  
atggcggccg ggagcatgcg acgtcggccc attcgcccta ta  
42

<210> 77  
<211> 14  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic Construct

<400> 77

Met Ala Ala Gly Ser Met Arg Arg Arg Pro Ile Arg Pro Ile  
1 5 10

<210> 78  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Construct

<400> 78  
atgcgacgtc ggcccattcg ccctata  
27

<210> 79  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic Construct

<400> 79

Met Arg Arg Arg Pro Ile Arg Pro Ile  
1 5

<210> 80

<211> 15

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 80

atgacacaat ttcct  
15

<210> 81

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 81

Met Thr Gln Phe Pro  
1 5

<210> 82

<211> 3787

<212> DNA

<213> Homo sapiens

<400> 82

tggagtgggc tgagggactc cactagaggc tgtccatctg gattccctgc ctccctagga  
60

gcccaacaga gcaaagcaag tgggcacaag gagtatgggtt ctaacgtgat tgggggtcatg  
120

aagacgttgc tgttggactt ggctttgtgg tcaactgctct tccagcccgg gtggctgtcc

180

tttagttccc aggtgagtca gaactgccac aatggcagct atgaaatcag cgtcctgatg  
240

atgggcaact cagcctttgc agagcccctg aaaaacttgg aagatgcggt gaatgagggg  
300

ctggaaatag tgagaggacg tctgcaaaat gctggcctaa atgtgactgt gaacgctact  
360

ttcatgtatt cggatgggtct gattcataac tcaggcgact gccggagtag cacctgtgaa  
420

ggcctcgacc tactcaggaa aatttcaaata gcacaacgga tgggctgtgt cctcataggg  
480

ccctcatgta catactccac cttccagatg taccttgaca cagaattgag ctaccccatg  
540

atctcagctg gaagttttgg attgtcatgt gactataaag aaaccttaac caggctgatg  
600

tctccagcta gaaagttgat gtacttcttg gttaactttt ggaaaaccaa cgatctgccc  
660

ttcaaaaactt attcctggag cacttcgtat gtttacaaga atggtacaga aactgaggac  
720

tgtttctggg accttaatgc tctggaggct agcggttcct atttctccca cgaactcggc  
780

tttaagggtg tgtaagaca agataaggag tttcaggata tcttaatgga ccacaacagg  
840

aaaagcaatg tgattattat gtgtgggtgg ccagagttcc tctacaagct gaagggtgac  
900

cgagcagtgg ctgaagacat tgtcattatt ctagtggatc ttttcaatga ccagtacttg  
960

gaggacaatg tcacagcccc tgactatatg aaaaatgtcc ttgttctgac gctgtctcct  
1020

gggaattccc ttctaaatag ctctttctcc aggaatctat caccaacaaa acgagacttt  
1080

cgtcttgcct atttgaatgg aatcctcgtc tttggacata tgctgaagat atttcttgaa  
1140

aatggagaaa atattaccac ccccaaattt gctcatgcct tcaggaatct cacttttgaa  
1200

gggtatgacg gtccagtgac cttggatgac tgggggggatg ttgacagtac catgggtgctt  
1260

ctgtatacct ctgtggacac caagaaatac aagggttcttt tgacctatga taccacgta  
1320

aataagacct atcctgtgga tatgagcccc acattcactt ggaagaactc taaacttcct  
1380

aatgatatta caggccgggg cctcagatc ctgatgattg cagtcttcac cctcactgga  
1440

gctgtggtgc tgctcctgct cgtcgctctc ctgatgctca gaaaatatag aaaagattat  
1500

gaacttcgtc agaaaaaatg gtcccacatt cctcctgaaa atatctttcc tctggagacc  
1560

aatgagacca atcatgttag cctcaagatc gatgatgaca aaagacgaga tacaatccag  
1620

agactacgac agtgcaaata cgtcaaaaag cgagtgattc tcaaagatct caagcacaat  
1680

gatggttaatt tcaactgaaaa acagaagata gaattgaaca agttgcttca gattgactat  
1740

tacaccctaa ccaagttcta cgggacagtg aaactggata ccatgatctt cggggtgata  
1800

gaataactgtg agagaggatc cctccgggaa gttttaaatg acacaatttc ctaccctgat  
1860

ggcacattca tggattggga gttaagatc tctgtcttgt atgacattgc taagggaatg  
1920

tcatatctgc actccagtaa gacagaagtc catggtcgtc tgaaatctac caactgcgta  
1980



gtggacagta gaatggtggt gaagatcact gattttggct gcaattccat tttgcctcca  
2040

aaaaaggacc tgtggacagc tccagagcac ctccgccaag ccaacatctc tcagaaagga  
2100

gatgtgtaca gctatgggat catcgcacag gagatcattc tgcggaaaga aaccttctac  
2160

actttgagct gtcgggaccg gaatgagaag attttcagag tggaaaattc caatggaatg  
2220

aaacccttcc gccagattt attcttgga acagcagagg aaaaagagct agaagtgtac  
2280

ctacttgtaa aaaactgttg ggaggaagat ccagaaaaga gaccagattt caaaaaaatt  
2340

gagactacac ttgccaaagat atttggactt tttcatgacc aaaaaaatga aagctatatg  
2400

gataccttga tccgacgtct acagctatat tctcgaaacc tggaacatct ggtagaggaa  
2460

aggacacagc tgtacaaggc agagaggac agggctgaca gacttaactt tatgttgctt  
2520

ccaaggctag tggtaaagtc tctgaaggag aaaggctttg tggagccgga actatatgag  
2580

gaagttacaa tctacttcag tgacattgta ggtttcta ctatctgcaa atacagcacc  
2640

cccatggaag tggaggacat gcttaatgac atctataaga gttttgacca cattgttgat  
2700

catcatgatg tctacaaggt ggaaaccatc ggtgatgcgt acatggtggc tagtggtttg  
2760

cctaagagaa atggcaatcg gcatgcaata gacattgcca agatggcctt ggaaatcctc  
2820

agcttcatgg ggacctttga gctggagcat cttcctggcc tcccaatatg gattcgcatt  
2880

ggagttcact ctggtccttg tgctgctgga gttgtgggaa tcaagatgcc tcgttattgt

2940

ctatttgag atacgggtcaa cacagcctct aggatggaat ccactggcct ccctttgaga  
3000

attcacgtga gtggctccac catagccatc ctgaagagaa ctgagtgcc gttcctttat  
3060

gaagtgagag gagaaacata cttaaaggga agaggaaatg agactaccta ctggctgact  
3120

gggatgaagg accagaaatt caacctgcc acccctccta ctgtggagaa tcaacagcgt  
3180

ttgcaagcag aattttcaga catgattgcc aactctttac agaaaagaca ggcagcaggg  
3240

ataagaagcc aaaaaccag acgggtagcc agctataaaa aaggcactct ggaatacttg  
3300

cagctgaata ccacagacaa ggagagcacc tattttttaa cctaaatgag gtataaggac  
3360

tcacacaaat taaaatacag ctgcactgag gccaggcacc ctcaggtgtc ctgaaagctt  
3420

actttcctga gacctcatga ggcagaaatg tcttaggctt ggctgccctg tttggaccat  
3480

ggactttctt tgcataatc agatgtgttc tcagtgaat aactaccttc cactctggaa  
3540

ccttattcca gcagttgttc caggagctt ctacctggaa aagaaaagaa tttcatttat  
3600

tttttgtttg tttattttta tcgtttttgt ttactggctt tccttctgta ttcataagat  
3660

tttttaaatt gtcataatta tattttaaat acccatcttc attaaagtat atttaactca  
3720

taatttttgc agaaaatatg ctatatatta ggcaagaata aaagctaaag gtttcccaaa  
3780

aaaaaaa  
3787